

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(I) APPLICANTS: Elmore, Michael James  
Mauchline, Margaret Lamble  
Minton, Nigel Peter  
Pasechnik, Vladimir Artymovich  
Titball, Richard William

(ii) TITLE OF INVENTION: Type F Botulinum Toxin and Use Thereof

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (To Be Assigned)  
(B) FILING DATE: 12-DEC-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/GB96/01409  
(B) FILING DATE: 12-JUN-1996  
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511909.5  
(B) FILING DATE: 12-JUN-1995  
(C) CLASSIFICATION:

(ix) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 1581.0200000

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

362250-28018630

(A) LENGTH: 431 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr  
1 5 10 15

Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn  
20 25 30

Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly  
35 40 45

Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser  
50 55 60

Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr  
65 70 75 80

Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro  
85 90 95

Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp  
100 105 110

Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn  
115 120 125

Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu  
130 135 140

Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys  
145 150 155 160

Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile  
165 170 175

Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly  
180 185 190

Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn  
195 200 205

Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu

210 215 220

Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro  
225 230 235 240

Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg  
245 250 255

Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn  
260 265 270

Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro  
275 280 285

Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile  
290 295 300

Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg  
305 310 315 320

Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr  
325 330 335

Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys  
340 345 350

Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val  
355 360 365

Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn  
370 375 380

Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala  
385 390 395 400

Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly  
405 410 415

Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn  
420 425 430

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr  
1 5 10 15

Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn  
20 25 30

Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly  
35 40 45

Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser  
50 55 60

Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr  
65 70 75 80

Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro  
85 90 95

Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp  
100 105 110

Cys Ile Arg Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn  
115 120 125

Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys  
1 5 10 15

Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile  
20 25 30

Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly

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35 40 45  
Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn  
50 55 60  
Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu  
65 70 75 80  
Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro  
85 90 95  
Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg  
100 105 110  
Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn  
115 120 125  
Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile  
1 5 10 15  
Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg  
20 25 30  
Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr  
35 40 45  
Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys  
50 55 60  
Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val  
65 70 75 80  
Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn

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85 90 95

Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala  
100 105 110

Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly  
115 120 125

Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn  
130 135 140

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TCATATACTA ATGATAAAAT TCTAATTITA TATTTTAATA AATTATATAA AAAAATTAAA 60  
GATAACTCTA TTITAGATAT GCGATATGAA AATAATAAAT TTATAGATAT CTCTGGATAT 120  
GGTTCAAATA TAAGCAATTAA TGGAGATGTA TATATTTATT CAACAAATAG AAATCAATT 180  
GGAATATATA GTAGTAAGCC TAGTGAAGTT AATATAGCTC AAAATAATGA TATTATATAC 240  
AATGGTAGAT ATCAAAATIT TAGTATTAGT TTCTGGGTAA GGATTCCTAA ATACTTCAAT 300  
AAAGTGAATC TTAATAATGA ATATACTATA ATAGATTGTA TAAGGAATAA TAATTCAAGGA 360  
TGGAAAATAT CACTTAATTAA TAATAAAAATA ATTTGGACTT TACAAGATAC TGCTGGAAAT 420  
AATCAAAAAC TAGTTTTTAA TTATACACAA ATGATTAGTA TATCTGATTA TATAAATAAA 480  
TGGATTTTTG TAACTATTAC TAATAATAGA TTAGGCAATT CTAGAATTAA CATCAATGGA 540  
AATTTAATAG ATGAAAAATC AATTCGAAT TTAGGTGATA TTCATGTTAG TGATAATATA 600  
TTATTTAAAA TTGTTGGTTG TAATGATACA AGATATGTTG GTATAAGATA TTTTAAAGTT 660  
TTTGATACGG AATTAGGTAA AACAGAAATT GAGACTTTAT ATAGTGATGA GCCAGATCCA 720  
AGTATCTTAA AAGACTTTTG GGGAAATTAT TTGTTATATA ATAAAAGATA TTATTTATTG 780

AATTACTAA GAACAGATAA GTCTATTACT CAGAATTCAA ACTTTCTAAA TATTAATCAA 840  
CAAAGAGGTG TTTATCAGAA ACCAAATATT TTTTCCAACA CTAGATTATA TACAGGAGTA 900  
GAAGTTATTAA TAAGAAAAAA TGGATCTACA GATATATCTA ATACAGATAA TTTTGTAGA 960  
AAAAATGATC TGGCATATAT TAATGTAGTA GATCGTGATG TAGAATATCG GCTATATGCT 1020  
GATATATCAA TTGCAAAACC AGAGAAAATA ATAAAATTAA TAAGAACATC TAATTCAAAC 1080  
AATAGCTTAG GTCAAATTAT AGTTATGGAT TCAATAGGAA ATAATTGCAC AATGAATTT 1140  
CAAAACAATA ATGGGGCAA TATAGGATTA CTAGGTTTC ATTCAAATAA TTTGGTTGCT 1200  
AGTAGTTGGT ATTATAACAA TATACGAAA AATACTAGCA GTAATGGATG CTTTTGGAGT 1260  
TTTATTCTA AAGAGCATGG ATGGCAAGAA AAC 1293

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGATCCATAT GTCTTACACT AACGACAAAA TCCTGATCCT GTACTTCAAC AACTGTACA 60  
AAAAAAATCAA AGACAACCTCT ATCCTGGACA TGCCTTACGA AAACAACAAA TTCATCGACA 120  
TCTCTGGCTA TGGTTCTAAC ATCTCTATCA ACGGTGACGT CTACATCTAC TCTACTAAC 180  
GCAACCAGTT CGGTATCTAC TCTTCTAAAC CGTCTGAAGT AAACATCGCT CAGAACAAACG 240  
ACATCATCTA CAACGGTCGT TACCAGAACT TCTCTATCTC TTTCTGGTT CGTATCCCGA 300  
AATACTTCAA CAAAGTTAAC CTGAACAAACG AATACACTAT CATCGACTGC ATCCGTAACA 360  
ACAACACTGG TTGGAAAATC TCTCTGAACt ACAACAAAAT CATCTGGACT CTGCAGGACA 420  
CTGCTGGTAA CAACCAGAAA CTGGTTTCA ACTACACTCA GATGATCTCT ATCTCTGACT 480  
ACATTAATAA ATGGATCTTC GTTACTATCA CTAACAACCG TCTGGGTAAAC TCTCGTATCT 540  
ACATCAACGG TAACCTGATC GATGAAAAAT CTATCTCTAA CCTGGGTGAC ATCCACGTT 600

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CTGACAAACAT CCTGTTCAAA ATCGTTGGTT GCAACGACAC GCGTTACGTT GGTATCCGTT	660
ACTTCAAAGT TTTCGACACT GAACTGGGTA AAACGTAAAT CGAAACTCTG TACTCTGACG	720
AACCGGACCC GTCTATCCTG AAAGACTTCT GGGGTAACTA CCTGCTGTAC AACAAACGTT	780
ACTACCTGCT GAACCTGCTC CGGACTGACA AATCTATCAC TCAGAACTCT AACTTCCTGA	840
ACATCAACCA GCAGCGTGGT GTTTATCAGA AACCTAATAT CTTCTCTAAC ACTCGTCTGT	900
ACACTGGTGT TGAAGTTATC ATCCGTAAAA ACGGTTCTAC TGACATCTCT AACACTGACA	960
ACTTCGTACG TAAAAACGAC CTGGCTTACA TCAACGTTGT TGACCGTGAC GTTGAATACC	1020
GTCTGTACGC TGACATCTCT ATCGCTAAC CGGAAAAAAAT CATCAAACGT ATCCGTACTT	1080
CTAACTCTAA CAACTCTCTG GGTCAGATCA TCGTTATGGA CTCGATCGGT AACAACTGCA	1140
CTATGAACCTT CCAGAACAAAC AACGGTGGTA ACATCGGTCT GCTGGGTTTC CACTCTAACCA	1200
ACCTGGTTGC TTCTTCTTGG TACTACAACA ACATCCGTAA AAACACTTCT TCTAACGGTT	1260
GCTTCTGGTC TTTCATCTCT AAAGAACACG GTTGGCAGGA AAACATAATCT AGA	1313

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#### ABSTRACT

The present invention relates to a polypeptide free of toxin activity which gives protection against botulinum type F toxin. The invention also relates to a fusion protein comprising a fragment of a toxin molecule and a purification moiety which enables purification of the fragment from solution. The invention also relates to pharmaceutical compositions comprising the polypeptide or the fusion protein, vaccines comprising the polypeptide, methods of producing the present polypeptides, vaccines and pharmaceutical compositions, and methods of vaccinating a mammal against a botulinum toxin.

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